

## SEQUENCE LISTING

## Sequence Listing

<110> Nara Institute of Science, Technology, Research Institute of Innovative Technology  
for the Earth and Kinki University

<120> Transgenic plants

<130> C01F1576

<160> 17

<210> 1

<211> 358

<212> PRT

<213> *Spinacia oleracea* L

<220> Fructose-1,6-bisphosphatase

<223>

<400> 1

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		20						25					30		
Ala	Gly	Val	Ile	Asp	Ala	Glu	Leu	Thr	Ile	Val	Leu	Ser	Ser	Ile	Ser
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Leu	Ala	Cys	Lys	Gln	Ile	Ala	Ser	Leu	Val	Gln	Arg	Ala	Gly	Ile	Ser
		50					55				60				
Asn	Leu	Thr	Gly	Ile	Gln	Gly	Ala	Val	Asn	Ile	Gln	Gly	Glu	Asp	Gln
65				70					75					80	
Lys	Lys	Leu	Asp	Val	Val	Ser	Asn	Glu	Val	Phe	Ser	Ser	Cys	Leu	Arg
			85					90					95		
Ser	Ser	Gly	Arg	Thr	Gly	Ile	Ile	Ala	Ser	Glu	Glu	Glu	Asp	Val	Pro
			100					105					110		
Val	Ala	Val	Glu	Glu	Ser	Tyr	Ser	Gly	Asn	Tyr	Ile	Val	Val	Phe	Asp
			115					120					125		
Pro	Leu	Asp	Gly	Ser	Ser	Asn	Ile	Asp	Ala	Ala	Val	Ser	Thr	Gly	Ser
		130					135					140			
Ile	Phe	Gly	Ile	Tyr	Ser	Pro	Asn	Asp	Glu	Cys	Ile	Val	Asp	Ser	Asp
145				150					155					160	
His	Asp	Asp	Glu	Ser	Gln	Leu	Ser	Ala	Glu	Glu	Gln	Arg	Cys	Val	Val
			165					170					175		
Asn	Val	Cys	Gln	Pro	Gly	Asp	Asn	Leu	Leu	Ala	Ala	Gly	Tyr	Cys	Met
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Tyr	Ser	Ser	Ser	Val	Ile	Phe	Val	Leu	Thr	Ile	Gly	Lys	Gly	Val	Tyr

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195                      200                      205  
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 210                      225                      220  
 Lys Ile Gln Ile Pro Lys Ala Gly Lys Ile Tyr Ser Phe Asn Glu Gly  
 225                      230                      235                      240  
 Asn Tyr Lys Met Trp Asp Asp Lys Leu Lys Lys Tyr Met Asp Asp Leu  
 245                      250                      255  
 Lys Glu Pro Gly Glu Ser Gln Lys Pro Tyr Ser Ser Arg Tyr Ile Gly  
 260                      265                      270  
 Ser Leu Val Gly Asp Phe His Arg Thr Leu Leu Tyr Gly Gly Ile Tyr  
 275                      280                      285  
 Gly Tyr Pro Arg Asp Ala Lys Ser Lys Asn Gly Lys Leu Arg Leu Leu  
 290                      295                      300  
 Tyr Glu Cys Ala Pro Met Ser Phe Ile Val Glu Gln Ala Gly Gly Lys  
 305                      310                      315                      320  
 Gly Ser Asp Gly His Gln Arg Ile Leu Asp Ile Gln Pro Thr Glu Ile  
 325                      330                      335  
 His Gln Arg Val Pro Leu Tyr Ile Gly Ser Val Glu Glu Val Glu Lys  
 340                      345                      350  
 Leu Glu Lys Tyr Leu Ala  
 355

&lt;210&gt; 2

&lt;211&gt; 1074

&lt;212&gt; DNA

&lt;213&gt; Spinacia oleracea L

&lt;220&gt; Fructose-1,6-bisphosphatase

&lt;223&gt;

&lt;400&gt; 2

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<400> 3

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20								25				30			
Ile	Arg	Leu	Met	Met	Cys	Met	Gly	Glu	Ala	Leu	Arg	Thr	Ile	Gly	Phe
35								40				45			
Lys	Val	Arg	Thr	Ala	Ser	Cys	Gly	Gly	Thr	Gln	Cys	Val	Asn	Thr	Phe
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Gly	Asp	Glu	Gln	Leu	Ala	Ile	Asp	Val	Leu	Ala	Asp	Lys	Leu	Leu	Phe
65				70				75				80			
Glu	Ala	Leu	Asn	Tyr	Ser	His	Phe	Cys	Lys	Tyr	Ala	Cys	Ser	Glu	Glu
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Val	Ala	Phe	Asp	Pro	Leu	Asp	Gly	Ser	Ser	Ile	Val	Asp	Thr	Asn	Phe
115								120				125			
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130				135				140							
Val	Thr	Gly	Arg	Asp	Gln	Val	Ala	Ala	Ala	Met	Gly	Ile	Tyr	Gly	Pro
145				150				155				160			
Arg	Thr	Thr	Tyr	Val	Leu	Ala	Leu	Lys	Asp	Tyr	Pro	Gly	Thr	His	Glu
165								170				175			
Phe	Leu	Leu	Leu	Asp	Glu	Gly	Lys	Trp	Gln	His	Val	Lys	Glu	Thr	Thr
180								185				190			
Glu	Ile	Asn	Glu	Gly	Lys	Leu	Phe	Cys	Pro	Gly	Asn	Leu	Arg	Ala	Thr
195								200				205			
Ser	Asp	Asn	Ala	Asp	Tyr	Ala	Lys	Leu	Ile	Gln	Tyr	Tyr	Ile	Lys	Glu

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210                      215                      220  
 Lys Tyr Thr Leu Arg Tyr Thr Gly Gly Met Val Pro Asp Val Asn Gln  
 225                      230                      235                      240  
 Ile Ile Val Lys Glu Lys Gly Ile Phe Thr Asn Val Ile Ser Pro Thr  
                     245                      250                      255  
 Ala Lys Ala Lys Leu Arg Leu Leu Phe Glu Val Ala Pro Leu Gly Phe  
                     260                      265                      270  
 Leu Ile Glu Lys Ala Gly Gly His Ser Ser Glu Gly Thr Lys Ser Val  
                     275                      280                      285  
 Leu Asp Ile Glu Val Lys Asn Leu Asp Asp Arg Thr Gln Val Ala Tyr  
                     290                      295                      300  
 Gly Ser Leu Asn Glu Ile Ile Arg Phe Glu Lys Thr Leu Tyr Gly Ser  
 305                      310                      315                      320  
 Ser Arg Leu Glu Glu Pro Val Pro Val Gly Ala Ala Ala  
                     325                      330

&lt;210&gt; 4

&lt;211&gt; 999

&lt;212&gt; DNA

<213> *Spinacia oleracea* L

&lt;220&gt; Sedoheptulose-1,7-bisphosphatase

&lt;223&gt;

&lt;400&gt; 4

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&lt;210&gt; 5

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&lt;211&gt; 356

&lt;212&gt; PRT

&lt;213&gt; Synechococcus

&lt;220&gt; fructose-1,6-bisphosphatase/sedoheptulose-1,7-bisphosphatase from Synechococcus

PCC 7942

&lt;223&gt;

&lt;400&gt; 5

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Met Glu Lys Thr Ile Gly Leu Glu Ile Ile Glu Val Val Glu Gln Ala
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      20              25              30
Asp Arg Val Ala Val Glu Ala Met Arg Val Arg Met Asn Gln Val Glu
      35              40              45
Met Leu Gly Arg Ile Val Ile Gly Glu Gly Glu Arg Asp Glu Ala Pro
      50              55              60
Met Leu Tyr Ile Gly Glu Glu Val Gly Ile Tyr Arg Asp Ala Asp Lys
      65              70              75              80
Arg Ala Gly Val Pro Ala Gly Lys Leu Val Glu Ile Asp Ile Ala Val
      85              90              95
Asp Pro Cys Glu Gly Thr Asn Leu Cys Ala Tyr Gly Gln Pro Gly Ser
      100             105             110
Met Ala Val Leu Ala Ile Ser Glu Lys Gly Gly Leu Phe Ala Ala Pro
      115             120             125
Asp Phe Tyr Met Lys Lys Leu Ala Ala Pro Pro Ala Ala Lys Gly Lys
      130             135             140
Glu Thr Ser Ile Lys Ser Ala Thr Glu Asn Leu Lys Ile Leu Ser Glu
      145             150             155             160
Cys Leu Asp Arg Ala Ile Asp Glu Leu Val Val Val Val Met Asp Arg
      165             170             175
Pro Arg His Lys Glu Leu Ile Gln Glu Ile Arg Gln Ala Gly Ala Arg
      180             185             190
Val Arg Leu Ile Ser Asp Gly Asp Val Ser Ala Ala Ile Ser Cys Gly
      195             200             205
Phe Ala Gly Thr Asn Thr His Ala Leu Met Gly Ile Gly Ala Ala Pro
      210             215             220
Glu Gly Val Ile Ser Ala Ala Ala Met Arg Cys Leu Gly Gly His Phe
      225             230             235             240
Gln Gly Gln Leu Ile Tyr Asp Pro Glu Val Val Lys Thr Gly Leu Ile
      245             250             255
Gly Glu Ser Arg Glu Ser Asn Ile Ala Arg Leu Gln Glu Met Gly Ile

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260	265	270
Thr Asp Pro Asp Arg Val Tyr Asp	Ala Asn Glu Leu Ala Ser Gly Gln	
275	280	285
Glu Val Leu Phe Ala Ala Cys Gly Ile Thr Pro Gly Leu Leu Met Glu		
290	295	300
Gly Val Arg Phe Phe Lys Gly Gly Ala Arg Thr Gln Ser Leu Val Ile		
305	310	315
Ser Ser Gln Ser Arg Thr Ala Arg Phe Val Asp Thr Val His Met Phe		
325	330	335
Asp Asp Val Lys Thr Val Ser Leu Pro Leu Ile Pro Asp Pro Lys Trp		
340	345	350
Arg Pro Glu Arg		
355		

&lt;210&gt; 6

&lt;211&gt; 1350

&lt;212&gt; DNA

&lt;213&gt; Synechococcus

<220> fructose-1,6-bisphosphatase/sedoheptulose-1,7-bisphosphatase from Synechococcus PCC. 7942

&lt;400&gt; 6

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&lt;210&gt; 7

&lt;211&gt; 133

&lt;212&gt; DNA

&lt;213&gt; Nicotiana tabacum

&lt;223&gt; psbA promoter

&lt;400&gt; 7

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ttaaataaac caa	133

&lt;210&gt; 8

&lt;211&gt; 159

&lt;212&gt; DNA

&lt;213&gt; Nicotiana tabacum

&lt;223&gt; rps16 terminator

&lt;400&gt; 8

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tatataactt tgaatgactt ttctcttcta tttttttgta ttccctccct ttccttttct	120
atttgtatth ttttatcatt gcttccattg aattactag	159

&lt;210&gt; 9

&lt;211&gt; 805

&lt;212&gt; DNA

&lt;213&gt; Escherichia coli

&lt;223&gt; aadA

&lt;400&gt; 9

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&lt;210&gt; 11

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&lt;212&gt; DNA

&lt;213&gt; Artificial sequence

&lt;223&gt; multi-cloning regions

&lt;400&gt; 11

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&lt;210&gt; 12

&lt;211&gt; 142

&lt;212&gt; DNA

&lt;213&gt; Nicotiana tabacum

&lt;223&gt; rrn promoter

&lt;400&gt; 12

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cttggataca gttgtaggga gg 142

&lt;210&gt; 13

&lt;211&gt; 390

&lt;212&gt; DNA

&lt;213&gt; Nicotiana tabacum

&lt;223&gt; psbA terminator

&lt;400&gt; 13

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tatcatigaa alaagaaaga agagctatat 390

&lt;210&gt; 14

&lt;211&gt; 5581

&lt;212&gt; DNA

&lt;213&gt; Artificial sequence

&lt;223&gt; pLD200

&lt;400&gt; 14

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&lt;210&gt; 15

&lt;211&gt; 1434

&lt;212&gt; DNA

<213> *Nicotiana tabacum*

&lt;223&gt; rbcL

&lt;400&gt; 15

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14/14

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&lt;210&gt; 16

&lt;211&gt; 705

&lt;212&gt; DNA

&lt;213&gt; Nicotiana tabacum

&lt;223&gt; accD

&lt;400&gt; 16

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&lt;210&gt; 17

&lt;211&gt; 21

&lt;212&gt; DNA

&lt;213&gt; Artificial sequence

&lt;223&gt; polylinker

&lt;400&gt; 17

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21

&lt;210&gt; 18

&lt;211&gt; 7

&lt;212&gt; DNA

&lt;213&gt; Artificial sequence

&lt;223&gt; Shine-Dalgarno Sequence

&lt;400&gt; 18

aggaggu

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